



BLAST

NCBI's sequence similarity search tool designed to support analysis of nucleotide and protein databases.

[Overview](#)

[BLAST FAQs](#)

[New/Noteworthy](#)

NEW [PHI-BLAST](#)

[Manual](#)

[References](#)

[NCBI Home](#)

[NLM Home](#)

[NIH Home](#)

[Credits](#)

NEW The Old (ungapped) BLAST service has been moved to the bottom of the page. NCBI recommends the use of BLAST 2.0 (Gapped BLAST), as this is a newer, improved service.

BLAST 2.0

- [Basic BLAST search](#)
- [Advanced BLAST search](#)

Position Specific Iterated BLAST

- [PSI-BLAST search](#)

NEW Pattern Hit Initiated BLAST

- [PHI-BLAST search](#)

NEW BLAST 2 sequences against each other

- [BLAST 2 sequences](#)

Specialized BLAST pages

- [Unfinished microbial genomes](#) NEW
- [P. falciparum](#)
- [TIGR Tentative Human Consensus \(THC\) sequences](#)

Old (ungapped) BLAST page

- [Ungapped BLAST search](#)
-



Exhibit C

General NCBI information: <info@ncbi.nlm.nih.gov>

BLAST questions: <blast-help@ncbi.nlm.nih.gov>

NCBI **Advanced BLAST** **Entrez ?****Clear Input****Basic BLAST**Message
of the day ...**Gapped BLAST**
(BLAST version 2.0)
is now available!**Choose program to use and database to search:**Program **blastp** Database **nr**

The query sequence is filtered for low complexity regions by default.

Depending on server load your search may take several seconds to several minutes.

Note: Nothing will be returned until your search is complete.

Enter here your input data as **Sequence in FASTA format** **Submit Query**

```
ssqyrgvtfyrrtgrweshiwdcgkqvylggfdtahaaaraydraaikfrgveadinfn  
ddyddd1
```

Please read about FASTA format description

Advanced options for the BLAST server:

Expect **default** Cutoff **default** Matrix **default**
Strand **both** Filter **none** ☐ Histogram ☐ NCBI-gi
Descriptions **default** Alignments **default**

Other advanced options:

The BLAST server may be very busy during the weekday, resulting in delays for users. The email option allows a user to receive the results quickly in a convenient form. If the HTML option is used, the results should be loaded into a web browser for viewing.

☐ Send reply to the Email address: ☐ In HTML format

Submit Query

Comments and suggestions to: < blast-help@ncbi.nlm.nih.gov >

Credits to: Sergei B. Shavirin

Acknowledgements to: Tom Madden and Jonathan Epstein

NCBI

BLAST Search Results

Entrez ?

Your query has been submitted, please wait for results

BLASTP 1.4.11 [24-Nov-97] [Build 24-Nov-97]

Reference: Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J. Lipman (1990). Basic local alignment search tool. J. Mol. Biol. 215:403-10.

Query= tmpseq_1
(67 letters)

Database: Non-redundant GenBank CDS
translations+PDB+SwissProt+SPupdate+PIR
331,304 sequences; 101,007,400 total letters.

Searching.....done

			High	Smallest	
			Score	Sum	
Sequences producing High-scoring Segment Pairs:				Probability	
				P(N)	N
<u>sp P47927 AP2_ARATH</u>	FLORAL HOMEOTIC PROTEIN APETALA2 /gi...	<u>368</u>	1.1e-43	1	
<u>gi 2944040</u>	(AF048900) indeterminate spikelet 1 ...	<u>345</u>	1.9e-40	1	
<u>gi 2281639</u>	(AF003100) AP2 domain containing pro...	<u>340</u>	9.5e-40	1	
<u>gi 1732031</u>	(U41466) AP2 DNA-binding domain prot...	<u>327</u>	6.4e-38	1	
<u>gi 3402680</u>	(AC004697) putative floral homeotic ...	<u>319</u>	8.5e-37	1	
<u>gi 2098818</u>	(AF001012) GLOSSY15 [Zea mays]	<u>205</u>	9.0e-21	1	
<u>gi 2887500</u>	(AC002339) putative AP2 domain-conta...	<u>126</u>	1.3e-16	2	
<u>pir S71365</u>	AP2 domain-containing protein - Arab...	<u>116</u>	6.6e-16	2	
<u>gi 1171429</u>	(U44028) CKC [Arabidopsis thaliana]	<u>116</u>	6.6e-16	2	
<u>gnl PID e1188628</u>	(Z47554) orf [Zea mays]	<u>123</u>	3.2e-15	2	
<u>pir S54116</u>	hypothetical protein - maize	<u>123</u>	3.0e-09	1	
<u>gi 2281641</u>	(AF003101) AP2 domain containing pro...	<u>112</u>	1.1e-07	1	
<u>gi 2281637</u>	(AF003099) AP2 domain containing pro...	<u>110</u>	2.0e-07	1	
<u>gnl PID d1007901</u>	(D38125) EREBP-4 [Nicotiana tabacum]	<u>110</u>	2.0e-07	1	
<u>gi 3617742</u>	(AC005687) RAP2.6 [Arabidopsis thali...	<u>110</u>	2.0e-07	1	
<u>gi 1903358</u>	(AC000104) Similar to Nicotiana EREB...	<u>106</u>	7.4e-07	1	
<u>gnl PID d1033384</u>	(AB008107) ethylene responsive eleme...	<u>105</u>	1.0e-06	1	
<u>gi 2529675</u>	(AC002535) putative AP2 domain conta...	<u>101</u>	1.1e-06	2	
<u>gi 2281635</u>	(AF003098) AP2 domain containing pro...	<u>100</u>	2.7e-06	2	
<u>gnl PID d1033383</u>	(AB008106) ethylene responsive eleme...	<u>100</u>	2.8e-06	2	
<u>gi 1707016</u>	(U78721) cadmium-induced protein iso...	<u>101</u>	3.7e-06	1	
<u>gi 2281629</u>	(AF003095) AP2 domain containing pro...	<u>101</u>	3.7e-06	1	
<u>gi 2213783</u>	(U89256) Pti5 [Lycopersicon esculentum]	<u>100</u>	5.1e-06	1	
<u>gnl PID d1007900</u>	(D38124) EREBP-3 [Nicotiana tabacum]	<u>97</u>	7.3e-06	2	
<u>gi 1732406</u>	(U81157) S25-XP1 DNA binding protein...	<u>98</u>	9.8e-06	1	
<u>gi 3600050</u>	(AF080120) contains similarity to AP...	<u>95</u>	1.3e-05	2	
<u>gnl PID d1032484</u>	(AB013301) ethylene responsive eleme...	<u>97</u>	1.4e-05	1	
<u>gnl PID d1033382</u>	(AB008105) ethylene responsive eleme...	<u>97</u>	1.4e-05	1	
<u>gnl PID e327065</u>	(Z97343) EREBP-4 homolog [Arabidopsi...	<u>97</u>	1.4e-05	1	
<u>gi 2213785</u>	(U89257) Pti6 [Lycopersicon esculentum]	<u>95</u>	1.5e-05	2	
<u>gi 2281649</u>	(AF003105) AP2 domain containing pro...	<u>96</u>	1.9e-05	1	
<u>gnl PID d1033380</u>	(AB008103) ethylene responsive eleme...	<u>96</u>	1.9e-05	1	
<u>gi 3342211</u>	(U89255) Pti4 [Lycopersicon esculentum]	<u>93</u>	4.9e-05	1	

gi 3264767	(AF071893) AP2 domain containing pro...	93	4.9e-05	1
gi 3065895	(AF058827) TSI1 [Nicotiana tabacum]	91	5.4e-05	2
gi 1688233	(U77655) DNA binding protein homolog...	74	8.0e-05	3
gnl PID d1007902	(D38126) EREBP-2 [Nicotiana tabacum]	91	9.5e-05	1
gi 2344900	(AC002388) EREBP isolog [Arabidopsis...	90	0.00013	1
gi 2281633	(AF003097) AP2 domain containing pro...	90	0.00013	1
gnl PID d1033381	(AB008104) ethylene responsive eleme...	88	0.00025	1
gnl PID e1287891	(AL022605) putative protein [Arabido...	88	0.00025	1
gnl PID e353340	(AJ001911) putative Ckc2 [Arabidopsi...	88	0.00025	1
gi 2281631	(AF003096) AP2 domain containing pro...	87	0.00034	1
gnl PID d1007899	(D38123) ERF1 [Nicotiana tabacum]	87	0.00034	1
gnl PID e1283534	(AL022197) transcriptional activator...	82	0.00039	2
gi 1899058	(U77378) transcriptional activator C...	82	0.00039	2
gi 2281643	(AF003102) AP2 domain containing pro...	86	0.00048	1
gnl PID e1249610	(AL021710) EREBP - like protein [Ara...	85	0.00066	1
gnl PID e353195	(Z99707) APETALA2 domain containing ...	83	0.00066	2
gi 2281647	(AF003104) AP2 domain containing pro...	81	0.00090	2
gnl PID d1034402	(AB013817) DREB1C [Arabidopsis thali...	84	0.00091	1
gnl PID e1283536	(AL022197) transcriptional activator...	84	0.00091	1
gi 2642430	(AC002391) putative AP2 domain conta...	81	0.0011	2
gi 2281645	(AF003103) AP2 domain containing pro...	83	0.0013	1
gnl PID d1034763	(AB007787) DREB1A [Arabidopsis thali...	82	0.0017	1
gnl PID d1034400	(AB013815) DREB1A [Arabidopsis thali...	82	0.0017	1
sp P42736 CDI3_ARATH	CADMIUM-INDUCED PROTEIN AS30 /pir S...	82	0.0017	1
gnl PID e1283535	(AL022197) transcriptional activator...	82	0.0017	1
gi 3702318	(AC005397) putative Ap2 domain prote...	81	0.0024	1
gnl PID e1283544	(AL022198) putative protein [Arabido...	81	0.0024	1
gi 3643601	(AC005395) hypothetical protein [Ara...	80	0.0033	1
gi 3540200	(AC004260) Similar to TINY [Arabidop...	79	0.0046	1
gi 3282693	(AF040959) AP2 domain family transcr...	79	0.0046	1
gi 2213612	(AC000103) F21J9.6 [Arabidopsis thal...	79	0.0046	1
gi 2281627	(AF003094) AP2 domain containing pro...	74	0.0076	2
gi 2344890	(AC002388) TINY transcription factor...	77	0.0087	1
gi 3395438	(AC004683) putative AP2 domain conta...	76	0.012	1
gi 2062174	(AC001645) transcription factor (TIN...	76	0.012	1
gnl PID d1034766	(AB007790) DREB2A [Arabidopsis thali...	75	0.017	1
gnl PID d1034767	(AB007791) DREB2B [Arabidopsis thali...	75	0.017	1
gnl PID e218696	(X94698) TINY [Arabidopsis thaliana]...	73	0.032	1
gi 3695034	(AF057373) ethylene response element...	72	0.043	1
sp P16146 PZ02_LUPPO	PPLZ02 PROTEIN /pir S11881 hypothet...	68	0.15	1
gi 47216	(X52071) unidentified product (195 A...	61	0.79	1
gi 485957	(Z32686) mrpD gene product [Proteus ...	58	0.98	1
gi 3033545	(AF055873) lignostilbene-alpha,beta-...	47	0.998	2
sp P34114 PHS2_DICDI	GLYCOGEN PHOSPHORYLASE 2 (GP2) /pir ...	56	0.9996	1
gi 2065531	(U78526) endo-1,4-beta-glucanase [Ly...	56	0.9996	1
sp P32932 VNS2_BTIVS	NONSTRUCTURAL PROTEIN NS2 /pir JC12...	56	0.9996	1
gnl PID d1021365	(D86222) glutamine synthetase [Pyroc...	56	0.9996	1

[sp|P47927|AP2_ARATH](#) FLORAL HOMEOTIC PROTEIN APETALA2 [gi|533709](#) (U12546)
 APETALA2 protein [Arabidopsis thaliana] [gnl|PID|e353193](#) (Z99707)
 APETALA2 protein [Arabidopsis thaliana]
 Length = 432

Score = 368 (171.8 bits), Expect = 1.1e-43, P = 1.1e-43
 Identities = 67/67 (100%), Positives = 67/67 (100%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNI 60
 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNI

Sbjct: 129 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNI 188

Query: 61 DDYDDDL 67
DDYDDDL

Sbjct: 189 DDYDDDL 195

Score = 40 (18.7 bits), Expect = 6.2e-09, Sum P(2) = 6.2e-09
Identities = 7/11 (63%), Positives = 10/11 (90%)

Query: 1 SSQYRGVTFYR 11
SS+YRGVT ++

Sbjct: 221 SSKYRGVTLHK 231

Score = 114 (53.2 bits), Expect = 6.2e-09, Sum P(2) = 6.2e-09
Identities = 25/43 (58%), Positives = 30/43 (69%)

Query: 25 KQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNIDYDDDL 67
K VYLG FDT AARAYD+AAIK G +A NF+ YD++L

Sbjct: 246 KYVYLGLFDTEVEAARAYDKAAIKCNGKDAVTNFDPSIYDEEL 288

gi|2944040 (AF048900) indeterminate spikelet 1 [Zea mays]
Length = 433

Score = 345 (161.1 bits), Expect = 1.9e-40, P = 1.9e-40
Identities = 61/67 (91%), Positives = 66/67 (98%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNI 60
SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRG++ADINF++

Sbjct: 110 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGLDADINFSL 169

Query: 61 DDYDDDL 67
DY+DDL

Sbjct: 170 SDYEDDL 176

Score = 40 (18.7 bits), Expect = 7.7e-08, Sum P(2) = 7.7e-08
Identities = 7/11 (63%), Positives = 10/11 (90%)

Query: 1 SSQYRGVTFYR 11
SS+YRGVT ++

Sbjct: 202 SSKYRGVTLHK 212

Score = 106 (49.5 bits), Expect = 7.7e-08, Sum P(2) = 7.7e-08
Identities = 22/40 (55%), Positives = 27/40 (67%)

Query: 25 KQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNIDYD 64
K +YLG FD+ AARAYDRAA++F G EA NF Y+

Sbjct: 227 KYIYLGLFDSEVEAARAYDRAALRFNGREAVTNFEPSSYN 266

gi|2281639 (AF003100) AP2 domain containing protein RAP2.7 [Arabidopsis
thaliana]
Length = 403

Score = 340 (158.7 bits), Expect = 9.5e-40, P = 9.5e-40
Identities = 60/67 (89%), Positives = 65/67 (97%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAARAYDRAAIKFRGVEADINFNI 60

Sbjct: 105 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGV+ADINF +
Query: 61 DDYDDDL 67
DY++D+
Sbjct: 165 GDYEEDM 171

Score = 40 (18.7 bits), Expect = 0.017, Sum P(2) = 0.017
Identities = 7/11 (63%), Positives = 10/11 (90%)

Query: 1 SSQYRGVTFYR 11
SS+YRGVT ++
Sbjct: 197 SSKYRGVTLHK 207

Score = 64 (29.9 bits), Expect = 0.017, Sum P(2) = 0.017
Identities = 12/28 (42%), Positives = 18/28 (64%)

Query: 40 RAYDRAAIKFRGVEADINFNIDYDDDL 67
+AYD+AAI G EA NF + Y +++
Sbjct: 222 KAYDKAAINTNGREAVTNFEMSSYQNEI 249

gi|1732031 (U41466) AP2 DNA-binding domain protein [Zea mays]
Length = 446

Score = 327 (152.7 bits), Expect = 6.4e-38, P = 6.4e-38
Identities = 58/67 (86%), Positives = 63/67 (94%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNI 60
SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTA AAARAYD+AAIKFRG+ ADINF +
Sbjct: 111 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAQAAARAYDQAAIKFRGLNADINFNL 170
Query: 61 DDYDDDL 67
DDY D++
Sbjct: 171 DDYKDEM 177

Score = 111 (51.8 bits), Expect = 1.5e-07, P = 1.5e-07
Identities = 24/43 (55%), Positives = 29/43 (67%)

Query: 25 KQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDDL 67
K VYLG +DT AA+AYD+AAIK G EA NF+ YD +L
Sbjct: 228 KYVYLGLYDTETEEAQAAYDKAAIKCYGKEAVTNFDAQSYDKEL 270

gi|3402680 (AC004697) putative floral homeotic protein [Arabidopsis thaliana]
Length = 236

Score = 319 (148.9 bits), Expect = 8.5e-37, P = 8.5e-37
Identities = 56/67 (83%), Positives = 62/67 (92%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNI 60
SS YRGVTFYRRTGRWESHIWDCGKQVYLGGFDTA+ AARAYDRAAI+FRG++ADINF +
Sbjct: 106 SSHYRGVTFYRRTGRWESHIWDCGKQVYLGGFDTAAYTAARAYDRAAIRFRGLQADINFIV 165
Query: 61 DDYDDDL 67
DDY D+
Sbjct: 166 DDYKQDI 172

gi|2098818 (AF001012) GLOSSY15 [Zea mays]
Length = 139

Score = 33 (15.4 bits), Expect = 2.0e-09, Sum P(3) = 2.0e-09
Identities = 6/11 (54%), Positives = 10/11 (90%)

Query: 1 SSQYRGVTFYR 11
SS++RGVT ++
Sbjct: 72 SSRFRGVTQHK 82

Score = 30 (14.0 bits), Expect = 2.0e-09, Sum P(3) = 2.0e-09
Identities = 4/9 (44%), Positives = 7/9 (77%)

Query: 12 RTGRWESHI 20
+ G+WE+ I
Sbjct: 82 KCGKWEARI 90

Score = 111 (51.8 bits), Expect = 2.0e-09, Sum P(3) = 2.0e-09
Identities = 24/43 (55%), Positives = 29/43 (67%)

Query: 25 KQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDDL 67
K VYLG +DT AA+AYD+AAIK G EA NF+ YD +L
Sbjct: 97 KYVYLGLYDTETEAQAAYDKAAIKCYGKEAVTNFDAQSYDKEL 139

Score = 205 (95.7 bits), Expect = 9.0e-21, P = 9.0e-21
Identities = 37/46 (80%), Positives = 42/46 (91%)

Query: 22 DCGKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDDL 67
DCGKQVYLGGFDTA AAARAYD+AAIKFRG+ ADINF +DDY D++
Sbjct: 1 DCGKQVYLGGFDTAQAAARAYDQAAIKFRGLNADINFNIDYDDDL 46

gi|2887500 (AC002339) putative AP2 domain-containing protein
[Arabidopsis thaliana]
Length = 436

Score = 84 (39.2 bits), Expect = 1.3e-16, Sum P(2) = 1.3e-16
Identities = 15/22 (68%), Positives = 19/22 (86%)

Query: 1 SSQYRGVTFYRRTGRWESHIWD 22
SS YRGVT +R TGR+E+H+WD
Sbjct: 68 SSIYRGVTRHRWTGRYEHLWD 89

Score = 126 (58.8 bits), Expect = 1.3e-16, Sum P(2) = 1.3e-16
Identities = 27/52 (51%), Positives = 32/52 (61%)

Query: 16 WESHIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDDL 67
W + GKQVYL +D AAARAYD AA+K+ G INF + DY DL
Sbjct: 93 WNQNQNKKGKQVYLGAAYDDEEAAARAYDLAALKYWGPGTLINFPVTDYTRDL 144

pir||S71365 AP2 domain-containing protein - Arabidopsis thaliana
gi|1209099 (U40256) AINTEGUMENTA [Arabidopsis thaliana] gi|1244708
(U41339) ANT [Arabidopsis thaliana]
Length = 555

Score = 89 (41.6 bits), Expect = 6.6e-16, Sum P(2) = 6.6e-16
Identities = 15/22 (68%), Positives = 20/22 (90%)

Query: 1 SSQYRGVTFYRRTGRWESHIWD 22
+SQYRGVT +R TGR+E+H+WD
Sbjct: 281 TSQYRGVTRHRWTGRYEHLWD 302

Score = 116 (54.2 bits), Expect = 6.6e-16, Sum P(2) = 6.6e-16
Identities = 21/44 (47%), Positives = 30/44 (68%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDL 67
G+QVYLGG+D AARAYD AA+K+ G NF+ ++Y ++
Sbjct: 314 GRQVYLGGYDMEKAARAYDLAALKYWGPTHTNFSANYQKEI 357

Score = 56 (26.1 bits), Expect = 3.1e-11, Sum P(2) = 3.1e-11
Identities = 10/20 (50%), Positives = 15/20 (75%)

Query: 1 SSQYRGVTFYRRTGRWESHI 20
+S YRGVT + + GRW++ I
Sbjct: 383 ASIYRGVTRHHQHGRWQARI 402

Score = 115 (53.7 bits), Expect = 3.1e-11, Sum P(2) = 3.1e-11
Identities = 25/42 (59%), Positives = 27/42 (64%)

Query: 25 KQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDD 66
K +YLG F T AA AYD AAIKFRG A NF+I YD D
Sbjct: 409 KDLYLGTFTGTQEEAAEAYDVAAIKFRGTNAVTFDITRYDVD 450

gi|1171429 (U44028) CKC [Arabidopsis thaliana]
Length = 555

Score = 89 (41.6 bits), Expect = 6.6e-16, Sum P(2) = 6.6e-16
Identities = 15/22 (68%), Positives = 20/22 (90%)

Query: 1 SSQYRGVTFYRRTGRWESHIWD 22
+SQYRGVT +R TGR+E+H+WD
Sbjct: 281 TSQYRGVTRHRWTGRYEHLWD 302

Score = 116 (54.2 bits), Expect = 6.6e-16, Sum P(2) = 6.6e-16
Identities = 21/44 (47%), Positives = 30/44 (68%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDL 67
G+QVYLGG+D AARAYD AA+K+ G NF+ ++Y ++
Sbjct: 314 GRQVYLGGYDMEKAARAYDLAALKYWGPTHTNFSANYQKEI 357

Score = 56 (26.1 bits), Expect = 3.1e-11, Sum P(2) = 3.1e-11
Identities = 10/20 (50%), Positives = 15/20 (75%)

Query: 1 SSQYRGVTFYRRTGRWESHI 20
+S YRGVT + + GRW++ I
Sbjct: 383 ASIYRGVTRHHQHGRWQARI 402

Score = 115 (53.7 bits), Expect = 3.1e-11, Sum P(2) = 3.1e-11
Identities = 25/42 (59%), Positives = 27/42 (64%)

Query: 25 KQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDD 66
K +YLG F T AA AYD AAIKFRG A NF+I YD D
Sbjct: 409 KDLYLGTFTGTQEEAAEAYDVAAIKFRGTNAVTFDITRYDVD 450

gnl|PID|e1188628 (Z47554) orf [Zea mays]
Length = 485

Score = 77 (36.0 bits), Expect = 3.2e-15, Sum P(2) = 3.2e-15
Identities = 13/22 (59%), Positives = 19/22 (86%)

Query: 1 SSQYRGVTFYRRTGRWESHIWD 22
+S YRGVT +R TGR+E+H+W+
Sbjct: 138 TSIYRGVTRHRWTGRYEHLWE 159

Score = 123 (57.4 bits), Expect = 3.2e-15, Sum P(2) = 3.2e-15
Identities = 23/44 (52%), Positives = 30/44 (68%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDDL 67
G+QVYLGG+D AARAYD AA+KF G NF + +Y+ +L
Sbjct: 171 GRQVYLGGYDKEEKAARAYDLAALKFWGPTTTTNFQVSNEYEKEL 214

Score = 56 (26.1 bits), Expect = 5.4e-10, Sum P(2) = 5.4e-10
Identities = 10/20 (50%), Positives = 15/20 (75%)

Query: 1 SSQYRGVTFYRRTGRWESHI 20
+S YRGVT + + GRW++ I
Sbjct: 240 ASIYRGVTRHHQHGRWQARI 259

Score = 106 (49.5 bits), Expect = 5.4e-10, Sum P(2) = 5.4e-10
Identities = 22/40 (55%), Positives = 26/40 (65%)

Query: 25 KQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYD 64
K +YLG F T AA AYD AAIKFRG+ A N ++ YD
Sbjct: 266 KDLYLGTFTSTQEEAAEAYDIAAIKFRGLNAVTNLDMSRYD 305

pir||S54116 hypothetical protein - maize
Length = 485

Score = 71 (33.2 bits), Expect = 0.061, P = 0.059
Identities = 12/26 (46%), Positives = 19/26 (73%)

Query: 1 SSQYRGVTFYRRTGRWESHIWDCGKQ 26
+S YRGVT + + GRW++ I CG++
Sbjct: 240 ASIYRGVTRHHQHGRWQARIRQCGRK 265

Score = 123 (57.4 bits), Expect = 3.0e-09, P = 3.0e-09
Identities = 23/44 (52%), Positives = 30/44 (68%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDDL 67
G+QVYLGG+D AARAYD AA+KF G NF + +Y+ +L
Sbjct: 171 GRQVYLGGYDKEEKAARAYDLAALKFWGPTTTTNFQVSNEYEKEL 214

gi|2281641 (AF003101) AP2 domain containing protein RAP2.8 [Arabidopsis thaliana]
Length = 334

Score = 112 (52.3 bits), Expect = 1.1e-07, P = 1.1e-07

Identities = 24/54 (44%), Positives = 35/54 (64%)

Query: 14 GRWESHIWDCGKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDDL 67
GRW + I++ ++V+LG F+ AAR+YD AA +FRG +A +NF D DL
Sbjct: 56 GRWGAQIYEKHQRVWLGTTFNEQEEAARSYDIAACRFRGRDAVVNFKNVLEDGDL 109

gi|2281637 (AF003099) AP2 domain containing protein RAP2.6 [Arabidopsis thaliana]
Length = 164

Score = 110 (51.4 bits), Expect = 2.0e-07, P = 2.0e-07
Identities = 21/33 (63%), Positives = 28/33 (84%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+V+LG F+TA AAARAYD AA++FRG +A +NF
Sbjct: 56 RVWLGTTFETAEEAAARAYDAAALRFRGSKAKLNF 88

gnl|PID|d1007901 (D38125) EREBP-4 [Nicotiana tabacum]
Length = 291

Score = 110 (51.4 bits), Expect = 2.0e-07, P = 2.0e-07
Identities = 22/38 (57%), Positives = 29/38 (76%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNID 61
G +V+LG FDTA AA+AYDRAA K RG +A +NF ++
Sbjct: 167 GTRVWLGTFTDAIEAAKAYDRAAFKLRGSKAIVNFPLE 204

gi|3617742 (AC005687) RAP2.6 [Arabidopsis thaliana]
Length = 192

Score = 110 (51.4 bits), Expect = 2.0e-07, P = 2.0e-07
Identities = 21/33 (63%), Positives = 28/33 (84%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+V+LG F+TA AAARAYD AA++FRG +A +NF
Sbjct: 84 RVWLGTTFETAEEAAARAYDAAALRFRGSKAKLNF 116

gi|1903358 (AC000104) Similar to Nicotiana EREBP-3 (gb|D38124).
[Arabidopsis thaliana]
Length = 133

Score = 106 (49.5 bits), Expect = 7.4e-07, P = 7.4e-07
Identities = 22/35 (62%), Positives = 26/35 (74%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G++V+LG FDTA AARAYDRAA RG A +NF
Sbjct: 42 GERVWLGTFTDAEDAARAYDRAAYSMRGKAAILNF 76

gnl|PID|d1033384 (AB008107) ethylene responsive element binding factor
5 [Arabidopsis thaliana]

Length = 300

Score = 105 (49.0 bits), Expect = 1.0e-06, P = 1.0e-06
Identities = 21/38 (55%), Positives = 28/38 (73%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNID 61
G +V+LG FDTA AARAYD AA + RG +A +NF ++
Sbjct: 178 GSRVWLGTFTDAIEAARAYDEAAFRLRGSKAILNFPLE 215

gi|2529675 (AC002535) putative AP2 domain containing protein
[Arabidopsis thaliana]
Length = 171

Score = 31 (14.5 bits), Expect = 1.1e-06, Sum P(2) = 1.1e-06
Identities = 7/17 (41%), Positives = 9/17 (52%)

Query: 11 RRTGRWESHIWDCGKQV 27
R G+W + I D K V
Sbjct: 56 RPWGKWAAEIRDPSKGV 72

Score = 101 (47.2 bits), Expect = 1.1e-06, Sum P(2) = 1.1e-06
Identities = 22/35 (62%), Positives = 26/35 (74%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F TA AARAYD AAIK RG +A +NF
Sbjct: 71 GVRVWLGTFTKTADEAARAYDVAAIKIRGRKAKLNF 105

gi|2281635 (AF003098) AP2 domain containing protein RAP2.5 [Arabidopsis thaliana]
Length = 213

Score = 30 (14.0 bits), Expect = 2.7e-06, Sum P(2) = 2.7e-06
Identities = 7/16 (43%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26
R GR+ + I D GK+
Sbjct: 31 RPWGRYAAEIRDPGKK 46

Score = 100 (46.7 bits), Expect = 2.7e-06, Sum P(2) = 2.7e-06
Identities = 21/33 (63%), Positives = 24/33 (72%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+V+LG FDTA AARAYD AA FRG +A NF
Sbjct: 48 RVWLGTFTDAEEAARAYDTAARDFRGAKAKTNF 80

gnl|PID|d1033383 (AB008106) ethylene responsive element binding factor
4 [Arabidopsis thaliana]
Length = 222

Score = 30 (14.0 bits), Expect = 2.8e-06, Sum P(2) = 2.8e-06
Identities = 7/16 (43%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26
R GR+ + I D GK+

Sbjct: 31 RPWGRYAAEIRDPGKK 46

Score = 100 (46.7 bits), Expect = 2.8e-06, Sum P(2) = 2.8e-06
Identities = 21/33 (63%), Positives = 24/33 (72%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+V+LG FDTA AARAYD AA FRG +A NF
Sbjct: 48 RVWLGTFTDAEEAARAYDTAARDFRGAKAKTNF 80

gi|1707016 (U78721) cadmium-induced protein isolog [Arabidopsis thaliana]
Length = 218

Score = 101 (47.2 bits), Expect = 3.7e-06, P = 3.7e-06
Identities = 20/33 (60%), Positives = 26/33 (78%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+V+LG FDTA AA AYD+AA +FRG +A +NF
Sbjct: 93 RVWLGTFTDAEEAALAYDKAAFEFRGHKAKLNF 125

gi|2281629 (AF003095) AP2 domain containing protein RAP2.2 [Arabidopsis thaliana]
Length = 246

Score = 101 (47.2 bits), Expect = 3.7e-06, P = 3.7e-06
Identities = 20/35 (57%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G + +LG FDTA AARAYD AA + RG +A +NF
Sbjct: 16 GSREWLGTFTDAEEAARAYDAAARRIRGTKAKVNF 50

gi|2213783 (U89256) Pti5 [Lycopersicon esculentum]
Length = 161

Score = 100 (46.7 bits), Expect = 5.1e-06, P = 5.1e-06
Identities = 20/35 (57%), Positives = 26/35 (74%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AA AYDRAA + RG +A +NF
Sbjct: 81 GARVWLGTFTDAEEAALAYDRAAFMRGAKALLNF 115

gnl|PID|d1007900 (D38124) EREBP-3 [Nicotiana tabacum]
Length = 225

Score = 30 (14.0 bits), Expect = 7.3e-06, Sum P(2) = 7.3e-06
Identities = 7/16 (43%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26
R GR+ + I D GK+
Sbjct: 33 RPWGRYAAEIRDPGKK 48

Score = 97 (45.3 bits), Expect = 7.3e-06, Sum P(2) = 7.3e-06
Identities = 20/33 (60%), Positives = 25/33 (75%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+V+LG FDTA AA+AYD AA +FRG +A NF
Sbjct: 50 RVWLGTFTDAEEAAKAYDTAAREFRGPKAKTNF 82

gi|1732406 (U81157) S25-XP1 DNA binding protein [Nicotiana tabacum]
Length = 277

Score = 98 (45.8 bits), Expect = 9.8e-06, P = 9.8e-06
Identities = 20/44 (45%), Positives = 28/44 (63%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDYDDDL 67
G +V+LG FD+ AAA AYD+AA RG A +NF ++ + L
Sbjct: 114 GVRVWLGTFDSPAAAALAYDQAAFLMRGTSAILNFPVETVQESL 157

gi|3600050 (AF080120) contains similarity to AP2 domain containing
proteins [Arabidopsis thaliana]
Length = 287

Score = 31 (14.5 bits), Expect = 1.3e-05, Sum P(2) = 1.3e-05
Identities = 6/17 (35%), Positives = 10/17 (58%)

Query: 11 RRTGRWESHIWDCGKQV 27
R G+W + I D ++V
Sbjct: 93 RPWGKWAAEIRDPSRRV 109

Score = 95 (44.4 bits), Expect = 1.3e-05, Sum P(2) = 1.3e-05
Identities = 19/33 (57%), Positives = 24/33 (72%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+V+LG FDTA AA YD AAI+ RG A++NF
Sbjct: 110 RVWLGTFTDAEEAAIVYDNAAIQLRGPNAELNF 142

gnl|PID|d1032484 (AB013301) ethylene responsive element binding factor
[Arabidopsis thaliana]
Length = 281

Score = 97 (45.3 bits), Expect = 1.4e-05, P = 1.4e-05
Identities = 19/38 (50%), Positives = 28/38 (73%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNID 61
G +V+LG F+TA AARAYD+ A + RG +A +NF ++
Sbjct: 159 GTRVWLGTFTETAIEAARAYDKEAFRLRGSKAILNFPLE 196

gnl|PID|d1033382 (AB008105) ethylene responsive element binding factor
3 [Arabidopsis thaliana]
Length = 225

Score = 97 (45.3 bits), Expect = 1.4e-05, P = 1.4e-05
Identities = 21/36 (58%), Positives = 25/36 (69%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNID 61

+V+LG FD+A AARRAYD AA RG +A NF ID
Sbjct: 51 RVWLGTFSAEAAAYDSAARNLRGPKAKTNFPID 86

gnl|PID|e327065 (Z97343) EREBP-4 homolog [Arabidopsis thaliana]
Length = 603

Score = 97 (45.3 bits), Expect = 1.4e-05, P = 1.4e-05
Identities = 19/38 (50%), Positives = 28/38 (73%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNID 61
G +V+LG F+TA AARRAYD+ A + RG +A +NF ++
Sbjct: 159 GTRVWLGTTFETAIEAARAYDKEAFRLRGSKAILNFPLE 196

gi|2213785 (U89257) Pti6 [Lycopersicon esculentum]
Length = 248

Score = 30 (14.0 bits), Expect = 1.5e-05, Sum P(2) = 1.5e-05
Identities = 6/12 (50%), Positives = 7/12 (58%)

Query: 11 RRTGRWESHIWD 22
R GRW + I D
Sbjct: 104 RPWGRWAAEIRD 115

Score = 95 (44.4 bits), Expect = 1.5e-05, Sum P(2) = 1.5e-05
Identities = 18/37 (48%), Positives = 26/37 (70%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNI 60
GK+V+LG +DT AA YD+AA+K +G +A NF +
Sbjct: 119 GKRVLGTGYDTPEEAAVVYDKAAVKLKGPDAVTNFPV 155

gi|2281649 (AF003105) AP2 domain containing protein RAP2.12
[Arabidopsis thaliana]
Length = 317

Score = 96 (44.8 bits), Expect = 1.9e-05, P = 1.9e-05
Identities = 19/35 (54%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +++LG F TA AARRAYD AA + RG +A +NF
Sbjct: 105 GARIWLGTFTKTAEEAARAYDAAARRIRGSKAKVNF 139

gnl|PID|d1033380 (AB008103) ethylene responsive element binding factor
1 [Arabidopsis thaliana]
Length = 266

Score = 96 (44.8 bits), Expect = 1.9e-05, P = 1.9e-05
Identities = 20/35 (57%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AA AYDRAA + RG A +NF
Sbjct: 168 GARVWLGTTFETAEDAALAYDRAAFMRGRSALLNF 202

gi|3342211 (U89255) Pti4 [Lycopersicon esculentum]
Length = 234

Score = 93 (43.4 bits), Expect = 4.9e-05, P = 4.9e-05
Identities = 18/35 (51%), Positives = 26/35 (74%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG ++TA AA AYD+AA + RG +A +NF
Sbjct: 128 GARVWLGTYETAEEAAIAYDKAAYRMRGSKAHLNF 162

gi|3264767 (AF071893) AP2 domain containing protein [Prunus armeniaca]
Length = 280

Score = 93 (43.4 bits), Expect = 4.9e-05, P = 4.9e-05
Identities = 19/35 (54%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AARAYD A + RG +A +NF
Sbjct: 33 GVRVWLGTFTNTAEEAARAYDSEARRIRGKKAKVNF 67

gi|3065895 (AF058827) TSI1 [Nicotiana tabacum]
Length = 251

Score = 30 (14.0 bits), Expect = 5.4e-05, Sum P(2) = 5.4e-05
Identities = 6/12 (50%), Positives = 7/12 (58%)

Query: 11 RRTGRWESHIWD 22
R GRW + I D
Sbjct: 113 RPWGRWAAEIRD 124

Score = 91 (42.5 bits), Expect = 5.4e-05, Sum P(2) = 5.4e-05
Identities = 18/35 (51%), Positives = 24/35 (68%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
GK+V+LG +DT AA YD AA+K +G +A NF
Sbjct: 128 GKRVLGLTYDTPPEAAIVYDAAVKLKGPDAVTNF 162

gi|1688233 (U77655) DNA binding protein homolog [Solanum tuberosum]
Length = 298

Score = 32 (14.9 bits), Expect = 8.0e-05, Sum P(3) = 8.0e-05
Identities = 7/17 (41%), Positives = 10/17 (58%)

Query: 11 RRTGRWESHIWDCGKQV 27
R G+W + I D K+V
Sbjct: 75 RPWGKWAAEIRDPRKRV 91

Score = 39 (18.2 bits), Expect = 8.0e-05, Sum P(3) = 8.0e-05
Identities = 8/13 (61%), Positives = 11/13 (84%)

Query: 26 QVYLGGFDTAHAA 38
+V+LG F+TA AA

Sbjct: 92 RVWLGTFTNTAEAA 104

Score = 74 (34.6 bits), Expect = 8.0e-05, Sum P(3) = 8.0e-05
Identities = 16/27 (59%), Positives = 19/27 (70%)

Query: 38 AARAYDRAAIKFRGVEADINFNIDDYD 64
AARAYDR A K RG +A +NF +D D

Sbjct: 103 AARAYDREARKIRGKKAKVNFNEDDD 129

gnl|PID|d1007902 (D38126) EREBP-2 [Nicotiana tabacum]
Length = 233

Score = 91 (42.5 bits), Expect = 9.5e-05, P = 9.5e-05
Identities = 18/35 (51%), Positives = 26/35 (74%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG ++TA AA AYD+AA + RG +A +NF

Sbjct: 121 GARVWLGTYETAEEAALAYDKAAYRMGRGSKALLNF 155

gi|2344900 (AC002388) EREBP isolog [Arabidopsis thaliana]
Length = 226

Score = 90 (42.0 bits), Expect = 0.00013, P = 0.00013
Identities = 18/35 (51%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG ++T AA AYDRAA + RG +A +NF

Sbjct: 114 GARVWLGTYETPEDAAVAYDRAAFQLRGSKAKLNF 148

gi|2281633 (AF003097) AP2 domain containing protein RAP2.4 [Arabidopsis thaliana]
Length = 229

Score = 90 (42.0 bits), Expect = 0.00013, P = 0.00013
Identities = 19/33 (57%), Positives = 24/33 (72%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+++LG FDTA AA AYD+AA K RG A +NF

Sbjct: 70 RLWLGTFTDTAEAAALAYDKAAYKLRGDFARLNF 102

gnl|PID|d1033381 (AB008104) ethylene responsive element binding factor
2 [Arabidopsis thaliana]
Length = 243

Score = 88 (41.1 bits), Expect = 0.00025, P = 0.00025
Identities = 19/35 (54%), Positives = 24/35 (68%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AA AYD AA + RG A +NF

Sbjct: 139 GARVWLGTFTETAEDAALAYDIAAFMRGRSALLNF 173

gnl|PID|e1287891 (AL022605) putative protein [Arabidopsis thaliana]
Length = 272

Score = 88 (41.1 bits), Expect = 0.00025, P = 0.00025
Identities = 19/33 (57%), Positives = 23/33 (69%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+++LG FDTA AA AYD AA K RG A +NF
Sbjct: 116 RLWLGTFTDAEEAAMAYDLAAYKLRGEFARLNF 148

gnl|PID|e353340 (AJ001911) putative Ckc2 [Arabidopsis thaliana]
Length = 246

Score = 88 (41.1 bits), Expect = 0.00025, P = 0.00025
Identities = 19/35 (54%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AA AYD AA + RG +A +NF
Sbjct: 101 GVRVWLGTFTNTAEEAAMAYDVAAKQIRGEKAKLNF 135

gi|2281631 (AF003096) AP2 domain containing protein RAP2.3 [Arabidopsis thaliana]
Length = 248

Score = 87 (40.6 bits), Expect = 0.00035, P = 0.00034
Identities = 19/35 (54%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG F+TA AA AYD AA + RG +A +NF
Sbjct: 100 GVRVWLGTFTNTAEEAAMAYDVAAKQIRGDKAKLNF 134

gnl|PID|d1007899 (D38123) ERF1 [Nicotiana tabacum]
Length = 236

Score = 87 (40.6 bits), Expect = 0.00035, P = 0.00034
Identities = 17/35 (48%), Positives = 25/35 (71%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
G +V+LG ++T AA AYD+AA + RG +A +NF
Sbjct: 127 GARVWLGTYETDEEAAIAYDKAAYRMRGSKAHLNF 161

gnl|PID|e1283534 (AL022197) transcriptional activator CBF1 [Arabidopsis thaliana]
gnl|PID|d1034401 (AB013816) DREB1B [Arabidopsis thaliana]
gnl|PID|d1034764 (AB007788) DREB1B [Arabidopsis thaliana]
Length = 213

Score = 32 (14.9 bits), Expect = 0.00039, Sum P(2) = 0.00039
Identities = 5/16 (31%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26
R +G+W S + + K+

Sbjct: 54 RNSGKWVSEVREPNNK 69

Score = 82 (38.3 bits), Expect = 0.00039, Sum P(2) = 0.00039
Identities = 17/33 (51%), Positives = 23/33 (69%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+++LG F TA AARA+D AA+ RG A +NF
Sbjct: 71 RIWLGTFTQAEMAARAHDVAALALRGRSACLNF 103

gi|1899058 (U77378) transcriptional activator CBF1 [Arabidopsis thaliana]
Length = 213

Score = 32 (14.9 bits), Expect = 0.00039, Sum P(2) = 0.00039
Identities = 5/16 (31%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26
R +G+W S + + K+
Sbjct: 54 RNSGKWVSEVREPNNK 69

Score = 82 (38.3 bits), Expect = 0.00039, Sum P(2) = 0.00039
Identities = 17/33 (51%), Positives = 23/33 (69%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58
+++LG F TA AARA+D AA+ RG A +NF
Sbjct: 71 RIWLGTFTQAEMAARAHDVAALALRGRSACLNF 103

gi|2281643 (AF003102) AP2 domain containing protein RAP2.9 [Arabidopsis thaliana]
Length = 94

Score = 86 (40.2 bits), Expect = 0.00048, P = 0.00048
Identities = 18/40 (45%), Positives = 25/40 (62%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINFNIDDYDD 65
+++LG + TA AAARAYD A RG A +NF + + D
Sbjct: 3 RIWLGSYKTAVAAARAYDTAVFYLRGPSARLNFPEEVFKD 42

gnl|PID|e1249610 (AL021710) EREBP - like protein [Arabidopsis thaliana]
Length = 303

Score = 85 (39.7 bits), Expect = 0.00066, P = 0.00066
Identities = 16/30 (53%), Positives = 22/30 (73%)

Query: 24 GKQVYLGGFDTAHAAARAYDRAAIKFRGVE 53
G +V+LG F TA AA AYD+AA++ RG +
Sbjct: 132 GVRVWLGTFTQAEAAAMAYDKAAVRIRGTQ 161

gnl|PID|e353195 (Z99707) APETALA2 domain containing protein homolog
[Arabidopsis thaliana]
Length = 196

Score = 29 (13.5 bits), Expect = 0.00066, Sum P(2) = 0.00066

Identities = 5/16 (31%), Positives = 10/16 (62%)

Query: 11 RRTGRWESHIWDCGKQ 26

R+ G+W + I + K+

Sbjct: 36 RKWGKWVAEIREPNKR 51

Score = 83 (38.8 bits), Expect = 0.00066, Sum P(2) = 0.00066

Identities = 16/33 (48%), Positives = 21/33 (63%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58

+++LG + T AAARAYD A RG A +NF

Sbjct: 53 RIWLGSYSTPEAAARAYDTAVFYLRGPSARLNF 85

gi|2281647 (AF003104) AP2 domain containing protein RAP2.11

[Arabidopsis thaliana]

Length = 255

Score = 31 (14.5 bits), Expect = 0.00090, Sum P(2) = 0.00090

Identities = 5/17 (29%), Positives = 11/17 (64%)

Query: 11 RRTGRWESHIWDCGKQV 27

R +G+W + I D +++

Sbjct: 30 RPSGKWVAEIKDTTQKI 46

Score = 81 (37.8 bits), Expect = 0.00090, Sum P(2) = 0.00090

Identities = 17/33 (51%), Positives = 21/33 (63%)

Query: 26 QVYLGGFDTAHAAARAYDRAAIKFRGVEADINF 58

+++LG F+TA AARAYD AA RG NF

Sbjct: 47 RMWLGTTFETAEEAARAYDEAACLLRGSNTRTNF 79

Parameters:

V=100

B=50

H=0

Lambda	K	H
0.324	0.140	0.453

Cutoff to enter 2nd pass: >= 38 (0.0 bits)

E	S	T1	T2	X1	X2	W	Gap
10.0		59	11	11	-15	-22	40 50

Database: Non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR

Posted date: Oct 22, 1998 7:43 AM

of letters in database: 101,007,400

of sequences in database: 331,304

Number of Hits to DB: 1st pass: 14105114, 2nd pass: 228077

Number of Sequences: 1st pass: 331304, 2nd pass: 2078

Number of extensions: 1st pass: 447103, 2nd pass: 171014

Number of successful extensions: 1st pass: 2078, 2nd pass: 2859

Number of sequences better than 10: 80

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